



## ORIGIN

MatC

10

D5

FEATURES	source
gene	<p>1. .2641</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="MGC:16795 IMAGE:385397"</p> <p>/tissue_type="Colon, adenocarcinoma"</p> <p>/clone_id="NIH_MGC_65"</p> <p>/lab_host="DH10B"</p> <p>/note="vector: pCMV-SPORT6"</p>
CDS	<p>1. .2641</p> <p>/gene="SEMA4B"</p> <p>/note="synonyms: SEMAC, KIAA1745, SemC"</p> <p>/db_xref="LocustID:10509"</p> <p>168. .1595</p> <p>/codon_start=1</p> <p>/product="sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B"</p> <p>/protein_id="AAH10701.1"</p> <p>/db_xref="GI:14715073"</p> <p>/translaton="MKDVORFSGLVSEKVNRETOOWYTVTHVPPEPGACITNSARSRKINSSILPDRVNLKDHIMDGVRSLILPQAPRVQVAVRPGLAHHTDVIVFLNGSDRLHKAVSVGRVPHIIEELQIFSSQIPQNLIDTRGLIYAASGVYQVAMANSKLRSGCDCLARDPYCAWSSGSCVSLVQPOLATPWQDITGASAKDICSISVVSFSPVPEKPEQVOVQFQPTVNTLACPLISNATRLMRNGAPVNASCHVPIGLGLIVGTQDLGEPOCWSLEBGFQDVLVASCPEVVDGADQDEGSGVLIISTRVSDPAGKASWAGPDRSGVYKKEFLVCTLFVAVLIPVFLIYRHSNSKVPILKQEGECVSHKTCGVVLPETRPINGGPPSTPLDHRGYQLSDSPPGARVFTSEKRPPLSIQISPEVSPSGPRPRRRLGSELRDSVY"</p>
misc_feature	<p>168. .602</p> <p>/note="Sema; Region: semaphorin domain"</p> <p>/db_xref="CDD:smart00630"</p> <p>654. .725</p> <p>/note="PSI; Region: domain found in Plexins, Semaphorins and Integrins"</p> <p>/db_xref="CDD:smart00423"</p>
misc_feature	<p>59.4%; Score 1587; DB 9; Length 2641; Best Local Similarity 99.7%; Pred. No. 1.4e-276; Matches 1590; Conservative 0; Mismatches 5; Indels 0; Gaps 0;</p>
REMARK	<p>NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a></p> <p>Contact: MGC help desk</p> <p>Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a></p> <p>Tissue Procurement: ATCC</p> <p>cDNA Library Preparation: Life Technologies, Inc.</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)</p> <p>DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center</p> <p>Center code: BCM-HGSC</p> <p>Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a></p> <p>Contact: <a href="mailto:amg@bcm.tmc.edu">amg@bcm.tmc.edu</a></p> <p>Gunnar, P. H., Garcia, A.M., Lu, X., Hulyk, S.W., Louie, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.</p>
COMMENT	<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a></p> <p>Series: IRAK Plate: 13 Row: C Column: 23</p> <p>This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.</p>
JOURNAL	<p>Location/Qualifiers</p> <p>1. .2641</p>
TITLE	<p>2 (bases 1 to 2641)</p>
AUTHORS	<p>Strausberg, R.</p>
REFERENCE	<p>12477932</p>
PUBMED	<p>2 (bases 1 to 2641)</p>
ORIGIN	<p>Query Match 59.4%; Score 1587; DB 9; Length 2641; Best Local Similarity 99.7%; Pred. No. 1.4e-276; Matches 1590; Conservative 0; Mismatches 5; Indels 0; Gaps 0;</p>

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 23:17:50 ; Search time 1274 Seconds  
(without alignments)  
10636.540 Million cell updates/sec

Title: US-09-981-318-15

Perfect score: 2673  
Sequence: 1 atgcccagcagcagcagcaggt.....tccgtgactctgtgtgtga 2673

Scoring table: IDENTITY NTC  
Gapco 10.0, Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2637.8	98.7	3781	10	US-09-946-374-252 Sequence 252, App
2	2637.8	98.7	3781	12	US-10-015-959A-252 Sequence 252, App
3	2637.8	98.7	3781	13	US-10-206-915-453 Sequence 453, App
4	2637.8	98.7	3781	13	US-10-199-670-453 Sequence 453, App
5	2637.8	98.7	3781	13	US-10-201-858-453 Sequence 453, App
6	2637.8	98.7	3781	13	US-10-205-890-453 Sequence 453, App
7	2637.8	98.7	3781	13	US-10-208-924-453 Sequence 453, App
8	2637.8	98.7	3781	13	US-10-201-853-453 Sequence 453, App
9	2637.8	98.7	3781	13	US-10-174-581-453 Sequence 453, App
10	2637.8	98.7	3781	13	US-10-176-483-453 Sequence 453, App
11	2637.8	98.7	3781	13	US-10-176-914-453 Sequence 453, App
12	2637.8	98.7	3781	13	US-10-176-914-453 Sequence 453, App
13	2637.8	98.7	3781	13	US-10-176-915-453 Sequence 453, App
14	2637.8	98.7	3781	13	US-10-006-485A-252 Sequence 252, App

15	2637.8	98.7	3781	13	US-10-013-907A-252 Sequence 252, App
16	2637.8	98.7	3781	13	US-10-015-499A-252 Sequence 252, App
17	2637.8	98.7	3781	13	US-10-176-484-453 Sequence 453, App
18	2637.8	98.7	3781	13	US-10-180-550-453 Sequence 453, App
19	2637.8	98.7	3781	13	US-10-183-014-453 Sequence 453, App
20	2637.8	98.7	3781	13	US-10-187-738-453 Sequence 453, App
21	2637.8	98.7	3781	13	US-10-187-740-453 Sequence 453, App
22	2637.8	98.7	3781	13	US-10-187-883-453 Sequence 453, App
23	2637.8	98.7	3781	13	US-10-194-460-453 Sequence 453, App
24	2637.8	98.7	3781	13	US-10-194-464-453 Sequence 453, App
25	2637.8	98.7	3781	13	US-10-194-484-453 Sequence 453, App
26	2637.8	98.7	3781	13	US-10-195-884-453 Sequence 453, App
27	2637.8	98.7	3781	13	US-10-195-896-453 Sequence 453, App
28	2637.8	98.7	3781	13	US-10-196-744-453 Sequence 453, App
29	2637.8	98.7	3781	13	US-10-196-755-453 Sequence 453, App
30	2637.8	98.7	3781	13	US-10-197-704-453 Sequence 453, App
31	2637.8	98.7	3781	13	US-10-197-710-453 Sequence 453, App
32	2637.8	98.7	3781	13	US-10-198-758-453 Sequence 453, App
33	2637.8	98.7	3781	13	US-10-198-766-453 Sequence 453, App
34	2637.8	98.7	3781	13	US-10-199-304-453 Sequence 453, App
35	2637.8	98.7	3781	13	US-10-199-309-453 Sequence 453, App
36	2637.8	98.7	3781	13	US-10-199-313-453 Sequence 453, App
37	2637.8	98.7	3781	13	US-10-199-313-453 Sequence 453, App
38	2637.8	98.7	3781	13	US-10-199-313-453 Sequence 453, App
39	2637.8	98.7	3781	13	US-10-199-313-453 Sequence 453, App
40	2637.8	98.7	3781	13	US-10-199-313-453 Sequence 453, App
41	2637.8	98.7	3781	13	US-10-201-329-453 Sequence 453, App
42	2637.8	98.7	3781	13	US-10-201-329-453 Sequence 453, App
43	2637.8	98.7	3781	13	US-10-202-412-453 Sequence 453, App
44	2637.8	98.7	3781	13	US-10-202-412-453 Sequence 453, App
45	2637.8	98.7	3781	13	US-10-206-928-453 Sequence 453, App

ALIGNMENTS

RESULT 1

US-09-946-374-252

Sequence 252 Application: US/0946374

Publication No. US20030073129A1

GENERAL INFORMATION:

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2830P1C1

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PRIOR APPLICATION NUMBER: 60/098716

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